Amendments to the Claims

Please cancel the withdrawn Claims 4, 5, 11-18 and 54. Please amend Claims 21, 26, 34 and 39. The Claim Listing below will replace all prior versions of the claims in the application:

Claim Listing

1-20. (Canceled)

21. (Currently Amended) ~~The Method of Claim 19,~~ A method for diagnosing the presence of a basement membrane disease in an individual, comprising detecting the presence of a mutation in exon 2 of the NPHS1 gene comprising the nucleic acid sequence of SEQ ID NO:1, wherein the mutation results in a premature stop codon in the exon and, wherein the mutation in exon 2 comprises a two base pair deletion of nucleotides 121-122 of the NPHS1 gene.

22. (Previously presented) The method of claim 21, wherein the NPHS1 gene is amplified prior to detecting the presence of the mutation in exon 2.

23. (Previously presented) The method of claim 22, wherein the amplification is by PCR and the primers used for amplification specifically amplify the exon 2 region of the NPHS1 gene.

24. (Previously presented) The method of claim 23, wherein the primers used for amplification comprise DNA sequences comprising SEQ ID NO:3 or SEQ ID NO:4.

25. (Canceled)

26. (Currently Amended) ~~The mutation of claim 25,~~ A method for diagnosing the presence of a basement membrane disease in an individual, comprising detecting the presence of a mutation in exon 26 of the NPHS1 gene comprising the nucleic acid sequence of SEQ ID NO:1, wherein the

mutation in exon 26 comprises a single base change, and wherein the single base pair change results in the nonsense mutation CGA->TGA.

27. (Currently Amended) The method of claim ~~25~~ 26, wherein the NPHS1 gene is amplified prior to detecting the presence of the mutation in exon 26.

28. (Previously presented) The method of claim 27, wherein the amplification is by PCR and the primers used for amplification specifically amplify the exon 26 region of the NPHS1 gene.

29. (Previously presented) The method of claim 28, wherein the primers used for amplification comprise DNA sequences comprising SEQ ID NO:5 or SEQ ID NO:6.

30. (Previously presented) The method of claim 29, wherein a novel restriction site is detected in the amplified product.

31. (Previously presented) The method of claim 30, wherein the novel restriction site is susceptible to digestion with DdeI.

32. (Canceled)

33. (Canceled)

34. (Currently Amended) ~~The method of claim 32,~~ A method of determining whether an individual is at risk for developing a congenital nephrotic syndrome of the Finnish Type, comprising analyzing a nucleic acid sample containing the NPHS1 gene comprising the nucleic acid sequence of SEQ ID NO:1, wherein the method comprises analyzing the exon 2 region of the NPHS1 gene, wherein an individual at risk for developing a congenital nephrotic syndrome has a mutation in exon 2, wherein the mutation in exon 2 comprises a two base pair ~~detection~~ deletion of nucleotides 121-122 of the NPHS1 gene.

35. (Previously presented) The method of claim 34 wherein the NPHS1 gene is amplified prior to detecting the presence of the mutation in exon 2.

36. (Previously presented) The method of claim 35, wherein the amplification is by PCR and the primers used for amplification specifically amplify the exon 2 region of the NPHS1 gene.

37. (Previously presented) The method of claim 36, wherein the primers used for amplification comprise DNA sequences selected from the group consisting of SEQ ID NO:3 or SEQ ID NO:4.

38. (Canceled)

39 (Currently Amended) ~~The mutation of claim 38.~~ A method of determining whether an individual is at risk for developing a congenital nephrotic syndrome of the Finnish Type, comprising analyzing a nucleic acid sample containing the NPHS1 gene comprising the nucleic acid sequence of SEQ ID NO:1, wherein the method comprises analyzing the exon 26 region of the NPHS1 gene, wherein an individual at risk for developing a congenital nephrotic syndrome has at least one mutation in exon 26, wherein the mutation in exon 26 comprises a single base pair change and, wherein the single base pair change results in the nonsense mutation CGA->TGA.

40. (Currently amended) The method of claim 39, wherein the NPHS1 gene ~~(SEQ ID NO:1)~~ is amplified prior to detecting the presence of the mutation in exon 26.

41. (Previously presented) The method of claim 40, wherein the amplification is by PCR and the primers used for amplification specifically amplify the exon 26 region of the NPHS1 gene.

42. (Previously presented) The method of claim 41, wherein the primers used for amplification comprise DNA sequences selected from the group consisting of SEQ ID NO:5 and SEQ ID NO:6.

43. (Previously presented) The method of claim 42, wherein a novel restriction site is detected in the amplified product.

44. (Previously presented) The method of claim 43, wherein the novel restriction site is susceptible to digestion with DdeI.

45. (Currently amended) A method for determining that an individual is not at risk for developing congenital nephritic syndrome of the Finnish Type, wherein the syndrome is associated with a mutation in exon 2 or exon 26 of the NPHS1 gene, wherein the method comprises analyzing the exon 2 or exon 26 region of the NPHS1 gene ~~encoded for by~~ comprising the nucleic acid sequence of SEQ ID NO:1, wherein the individual not at risk for developing the syndrome does not have a mutation in exon 2 or exon 26, wherein the mutation in exon 2 comprises a two base pair deletion of nucleotides 121-122 of the NPHS1 gene, and the mutation in exon 26 comprises a single base change resulting in the nonsense mutation CGA -> TGA.

46. (Canceled)

47. (Previously presented) The method of claim 45, wherein the NPHS1 gene is amplified prior to analysis.

48. (Previously presented) The method of claim 47, wherein the amplification is PCR amplification using primers comprising a DNA sequence selected from the group consisting of: SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6.

49. (Previously presented) A method for detecting the presence or absence of a mutation in the NPHS1 gene, comprising the steps of:

analyzing a nucleic acid test sample containing the NPHS1 gene encoded for by the nucleic acid sequence of SEQ ID NO:1 for at least one mutation in exon 2 or exon 26 of the gene;

comparing the results of the analysis of the test sample of step a) with the results of the analysis of a control sample, wherein the control sample comprises a NPHS1 gene encoded for by the nucleic acid sequence of SEQ ID NO:1 without a mutation in exon 2 or exon 26; and

determining the presence or absence of at least one mutation in exon 2 or exon 26 in the test sample.

50. (Canceled)

51. (Previously presented) The method of claim 49, wherein the mutation in exon 2 is a two base pair deletion and the mutation in exon 26 is a single base pair change, wherein either mutation results in a premature stop codon in the exon.

52. (Previously presented) The method of claim 49, wherein the NPHS1 gene is amplified prior to analysis.

53. (Previously presented) The method of claim 52, wherein the amplification is PCR amplification using primers comprising a DNA sequence selected from the group consisting of: SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6.

54. (Canceled)